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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/035,343

DATE: 01/17/2002

TIME: 15:50:46

Input Set : A:\2318-290-II.ST25.txt

Output Set: N:\CRF3\01172002\J035343.raw

ENTERED

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3 <110> APPLICANT: Myriad Genetics, Inc.
4   Cimbora, Daniel M.
5   Heichman, Karen
6   Bartel, Paul L.
8 <120> TITLE OF INVENTION: Protein-Protein Interactions
10 <130> FILE REFERENCE: 2318-290-II
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/035,343
C--> 12 <141> CURRENT FILING DATE: 2002-01-04
12 <150> PRIOR APPLICATION NUMBER: US 60/259,572
13 <151> PRIOR FILING DATE: 2001-01-04
15 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 40
21 <212> TYPE: DNA
C--> 22 <213> ORGANISM: Artificial
24 <220> FEATURE:
25 <223> OTHER INFORMATION: oligonucleotide primer
27 <400> SEQUENCE: 1
28 gcaggaaaca gctatgacca tacagtcagc ggccgccacc
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36 <220> FEATURE:
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39 <400> SEQUENCE: 2
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44 <211> LENGTH: 1633
45 <212> TYPE: DNA
46 <213> ORGANISM: Homo sapiens
48 <220> FEATURE:
49 <221> NAME/KEY: CDS
50 <222> LOCATION: (152)..(1633)
52 <400> SEQUENCE: 3
53 gaaagtttcg gttctgcccg gcggtggacc cacgagcgcg tgccaccatg gagtctgacc
55 actgctgagc agacagccac cgagggccga aattctgagc ctctctctgg acccaggcag
57 gagacataca gacaagaaag gcaaactcac c atg gcc tcc acc aat gca gag
58                               Met Ala Ser Thr Asn Ala Glu
59                               1           5
61 agc cag ctc cag aga atc atc cga gac ttg caa gat gct gtg aca gaa
62 Ser Gln Leu Gln Arg Ile Ile Arg Asp Leu Gln Asp Ala Val Thr Glu

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63	10	15	20		268
65	cta agc aaa gaa ttt cag gaa gca ggg gaa ccc atc acg gat gac agc				
66	Leu Ser Lys Glu Phe Gln Glu Ala Gly Glu Pro Ile Thr Asp Asp Ser				
67	25	30	35		316
69	acc agc ttg cat aaa ttt tct tat aaa ctt gag tat ctc ctg caa ttt				
70	Thr Ser Leu His Lys Phe Ser Tyr Lys Leu Glu Tyr Leu Leu Gln Phe				
71	40	45	50	55	
73	gat cag aaa gag aag gcc acc ctc ctg ggc aac aag aag gac tac tgg				364
74	Asp Gln Lys Glu Lys Ala Thr Leu Leu Gly Asn Lys Lys Asp Tyr Trp				
75	60	65	70		
77	gat tac ttc tgt gcc tgc ctg gcc aag gtg aaa gga gcc aat gat ggg				412
78	Asp Tyr Phe Cys Ala Cys Leu Ala Lys Val Lys Gly Ala Asn Asp Gly				
79	75	80	85		
81	atc cgc ttt gtc aag tct atc tca gag ctc cga aca tcc ttg ggg aaa				460
82	Ile Arg Phe Val Lys Ser Ile Ser Glu Leu Arg Thr Ser Leu Gly Lys				
83	90	95	100		
85	gga aga gca ttt att cgc tac tcc ttg gtg cac cag agg ttg gca gac				508
86	Gly Arg Ala Phe Ile Arg Tyr Ser Leu Val His Gln Arg Leu Ala Asp				
87	105	110	115		
89	acc tta cag cag tgc ttc atg aac acc aaa gtg acc agt gac tgg tac				556
90	Thr Leu Gln Gln Cys Phe Met Asn Thr Lys Val Thr Ser Asp Trp Tyr				
91	120	125	130	135	
93	tat gca aga agc ccc ttt ctg cag cca aag ctg agc tcg gac att gtg				604
94	Tyr Ala Arg Ser Pro Phe Leu Gln Pro Lys Leu Ser Ser Asp Ile Val				
95	140	145	150		
97	ggc caa ctc tat gag ctg act gag gtt cag ttt gac ctg gcg tcg agg				652
98	Gly Gln Leu Tyr Glu Leu Thr Glu Val Gln Phe Asp Leu Ala Ser Arg				
99	155	160	165		
101	ggc ttt gac ttg gat gct gcc tgg cca aca ttt gcc agg agg acg ctg				700
102	Gly Phe Asp Leu Asp Ala Ala Trp Pro Thr Phe Ala Arg Arg Thr Leu				
103	170	175	180		
105	acc act ggc tct tct gct tac ctg tgg aaa ccc cct agc cgc agc tcc				748
106	Thr Thr Gly Ser Ser Ala Tyr Leu Trp Lys Pro Pro Ser Arg Ser Ser				
107	185	190	195		
109	agc atg agc agc ttg gtg agc agc tac ctg cag act caa gag atg gtg				796
110	Ser Met Ser Ser Leu Val Ser Ser Tyr Leu Gln Thr Gln Glu Met Val				
111	200	205	210		
113	tcc aac ttt gac ctg aac agc ccc cta aac aac gag gca ttg gag ggc				844
114	Ser Asn Phe Asp Leu Asn Ser Pro Leu Asn Asn Glu Ala Leu Glu Gly				
115	220	225	230		
117	ttt gat gag atg cga cta gag ctg gac cag ttg gag gtg cgg gag aag				892
118	Phe Asp Glu Met Arg Leu Glu Leu Asp Gln Leu Glu Val Arg Glu Lys				
119	235	240	245		
121	cag cta cgg gag cgc atg cag cag ctg gac aga gag aac cag gag ctg				940
122	Gln Leu Arg Glu Arg Met Gln Gln Leu Asp Arg Glu Asn Gln Glu Leu				
123	250	255	260		
125	agg gca gct gtc agc cag caa ggg gag caa ctg cag aca gag agg gag				988
126	Arg Ala Ala Val Ser Gln Gln Gly Glu Gln Leu Gln Thr Glu Arg Glu				
127	265	270	275		

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129 agg ggg cgc act gca gcg gag gac aac gtt cgc ctc act tgc ttg gta      1036
130 Arg Gly Arg Thr Ala Ala Glu Asp Asn Val Arg Leu Thr Cys Leu Val      295
131 280      285      290
133 gct gag ctc cag aag cag tgg gag gtc acc cag gcc acc cag aac act      1084
134 Ala Glu Leu Gln Lys Gln Trp Glu Val Thr Gln Ala Thr Gln Asn Thr      310
135      300      305
137 gtg aag gag ctg cag aca tgc ctg cag gcc ctg gag cta gga gca gca      1132
138 Val Lys Glu Leu Gln Thr Cys Leu Gln Gly Leu Glu Leu Gly Ala Ala      325
139      315      320
141 gag aag gag gag gac tac cac aca gcc ctg cgg cgg ctg gag tcc atg      1180
142 Glu Lys Glu Glu Asp Tyr His Thr Ala Leu Arg Arg Leu Glu Ser Met      340
143      330      335
145 ctg cag ccc ttg gca cag gag ctt gag gcc aca cgg gac tca ctg gac      1228
146 Leu Gln Pro Leu Ala Gln Glu Leu Glu Ala Thr Arg Asp Ser Leu Asp      355
147      345      350
149 aag aaa aac cag cat tta gcc agc ttc cca gcc tgg cta gcc atg gct      1276
150 Lys Lys Asn Gln His Leu Ala Ser Phe Pro Gly Trp Leu Ala Met Ala      375
151 360      365      370
153 cag cag aag gca gat acg gca tca gac aca aag gcc cgg caa gaa cct      1324
154 Gln Gln Lys Ala Asp Thr Ala Ser Asp Thr Lys Gly Arg Gln Glu Pro      390
155      380      385
157 att ccc agt gat gcg gcc cag gag atg cag gag cta ggg gag aag ctt      1372
158 Ile Pro Ser Asp Ala Ala Gln Glu Met Gln Glu Leu Gly Glu Lys Leu      405
159      395      400
161 caa gcc cta gaa agg gag aga acc aag gtc gag gag gtc aac aga cag      1420
162 Gln Ala Leu Glu Arg Glu Arg Thr Lys Val Glu Glu Val Asn Arg Gln      420
163      410      415
165 cag agt gcc caa ctg gaa cag ctg gtc aag gag ctt cag ctg aaa gag      1468
166 Gln Ser Ala Gln Leu Glu Gln Leu Val Lys Glu Leu Gln Leu Lys Glu      435
167      425      430
169 gat gcc cgg gcc agc ctg gag cgc ctg gtg aag gag atg gcc cca ctc      1516
170 Asp Ala Arg Ala Ser Leu Glu Arg Leu Val Lys Glu Met Ala Pro Leu      455
171 440      445      450
173 cag gag gag ttg tct ggg aag gga cag gag gca gac cag ctc tgg cga      1564
174 Gln Glu Glu Leu Ser Gly Lys Gly Gln Glu Ala Asp Gln Leu Trp Arg      470
175      460      465
177 cgg ctg cag gag ttg ctg gcc cac acg agc tcc tgg gag gag gag cta      1612
178 Arg Leu Gln Glu Leu Leu Ala His Thr Ser Ser Trp Glu Glu Glu Leu      485
179      475      480
181 gca gag ttg agg cgg gag aaa      1633
182 Ala Glu Leu Arg Arg Glu Lys
183      490
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187 <211> LENGTH: 494
188 <212> TYPE: PRT
189 <213> ORGANISM: Homo sapiens
191 <400> SEQUENCE: 4
193 Met Ala Ser Thr Asn Ala Glu Ser Gln Leu Gln Arg Ile Ile Arg Asp
194 1      5      10      15

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197 Leu Gln Asp Ala Val Thr Glu Leu Ser Lys Glu Phe Gln Glu Ala Gly
198          20          25          30
201 Glu Pro Ile Thr Asp Asp Ser Thr Ser Leu His Lys Phe Ser Tyr Lys
202          35          40          45
205 Leu Glu Tyr Leu Leu Gln Phe Asp Gln Lys Glu Lys Ala Thr Leu Leu
206          50          55          60
209 Gly Asn Lys Lys Asp Tyr Trp Asp Tyr Phe Cys Ala Cys Leu Ala Lys
210 65          70          75          80
213 Val Lys Gly Ala Asn Asp Gly Ile Arg Phe Val Lys Ser Ile Ser Glu
214          85          90          95
217 Leu Arg Thr Ser Leu Gly Lys Gly Arg Ala Phe Ile Arg Tyr Ser Leu
218          100          105          110
221 Val His Gln Arg Leu Ala Asp Thr Leu Gln Gln Cys Phe Met Asn Thr
222          115          120          125
225 Lys Val Thr Ser Asp Trp Tyr Tyr Ala Arg Ser Pro Phe Leu Gln Pro
226          130          135          140
229 Lys Leu Ser Ser Asp Ile Val Gly Gln Leu Tyr Glu Leu Thr Glu Val
230 145          150          155          160
233 Gln Phe Asp Leu Ala Ser Arg Gly Phe Asp Leu Asp Ala Ala Trp Pro
234          165          170          175
237 Thr Phe Ala Arg Arg Thr Leu Thr Thr Gly Ser Ser Ala Tyr Leu Trp
238          180          185          190
241 Lys Pro Pro Ser Arg Ser Ser Ser Met Ser Ser Leu Val Ser Ser Tyr
242          195          200          205
245 Leu Gln Thr Gln Glu Met Val Ser Asn Phe Asp Leu Asn Ser Pro Leu
246          210          215          220
249 Asn Asn Glu Ala Leu Glu Gly Phe Asp Glu Met Arg Leu Glu Leu Asp
250 225          230          235          240
253 Gln Leu Glu Val Arg Glu Lys Gln Leu Arg Glu Arg Met Gln Gln Leu
254          245          250          255
257 Asp Arg Glu Asn Gln Glu Leu Arg Ala Ala Val Ser Gln Gln Gly Glu
258          260          265          270
261 Gln Leu Gln Thr Glu Arg Glu Arg Gly Arg Thr Ala Ala Glu Asp Asn
262          275          280          285
265 Val Arg Leu Thr Cys Leu Val Ala Glu Leu Gln Lys Gln Trp Glu Val
266          290          295          300
269 Thr Gln Ala Thr Gln Asn Thr Val Lys Glu Leu Gln Thr Cys Leu Gln
270 305          310          315          320
273 Gly Leu Glu Leu Gly Ala Ala Glu Lys Glu Glu Asp Tyr His Thr Ala
274          325          330          335
277 Leu Arg Arg Leu Glu Ser Met Leu Gln Pro Leu Ala Gln Glu Leu Glu
278          340          345          350
281 Ala Thr Arg Asp Ser Leu Asp Lys Lys Asn Gln His Leu Ala Ser Phe
282          355          360          365
285 Pro Gly Trp Leu Ala Met Ala Gln Gln Lys Ala Asp Thr Ala Ser Asp
286          370          375          380
289 Thr Lys Gly Arg Gln Glu Pro Ile Pro Ser Asp Ala Ala Gln Glu Met
290 385          390          395          400
293 Gln Glu Leu Gly Glu Lys Leu Gln Ala Leu Glu Arg Glu Arg Thr Lys

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294                               405                               410                               415
297 Val Glu Glu Val Asn Arg Gln Gln Ser Ala Gln Leu Glu Gln Leu Val
298                               420                               425                               430
301 Lys Glu Leu Gln Leu Lys Glu Asp Ala Arg Ala Ser Leu Glu Arg Leu
302                               435                               440                               445
305 Val Lys Glu Met Ala Pro Leu Gln Glu Glu Leu Ser Gly Lys Gly Gln
306                               450                               455                               460
309 Glu Ala Asp Gln Leu Trp Arg Arg Leu Gln Glu Leu Leu Ala His Thr
310 465                               470                               475                               480
313 Ser Ser Trp Glu Glu Glu Leu Ala Glu Leu Arg Arg Glu Lys
314                               485                               490

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VERIFICATION SUMMARY

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Input Set : A:\2318-290-II.ST25.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:22 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:34 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2